

RAW SEQUENCE LISTING

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Application Serial Number: 10/552,515
Source: PCT
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PCT

RAW SEQUENCE LISTING

DATE: 10/20/2005

PATENT APPLICATION: US/10/552,515

TIME: 09:40:29

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10202005\J552515.raw

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3 <110> APPLICANT: The Government of the United States of America as
4     represented by the Secretary of the Department of Health and
5     Human Services
6     Bera, Tapan K.
7     Pastan, Ira H.
8     Lee, Byungkook
10 <120> TITLE OF INVENTION: GENE EXPRESSED IN PROSTATE CANCER AND METHODS OF USE
12 <130> FILE REFERENCE: 4239-68223-02
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/552,515
C--> 14 <141> CURRENT FILING DATE: 2005-10-06
14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/10588
15 <151> PRIOR FILING DATE: 2004-04-05
17 <150> PRIOR APPLICATION NUMBER: 60/461,399
18 <151> PRIOR FILING DATE: 2003-04-08
20 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 933
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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35 1           5           10           15
38 Pro Thr Leu Cys Pro Ala Val Arg Thr Gly Leu Tyr Cys Arg Asp Gln
39           20           25           30
42 Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr Ser Ser Gly Ser
43           35           40           45
46 His Cys Ala Arg Ser Arg Met Leu Arg Arg Arg Ala Gln Glu Glu Asp
47           50           55           60
50 Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys Arg Gly
51 65           70           75           80
54 Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln Gln Ala
55           85           90           95
58 Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Ala Asp Phe
59           100          105          110
62 Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp Ser
63           115          120          125
66 Ala Ala Arg Asp Arg Thr Asp Met His Arg Thr Trp Arg Glu Thr Phe
67           130          135          140
70 Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp Val
71 145          150          155          160

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74 Gln Asp Gly Asn Thr Thr Val His Tyr Ala Leu Leu Ser Ala Ser Trp
75                      165                      170                      175
78 Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro Leu
79                      180                      185                      190
82 Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu Ala
83                      195                      200                      205
86 Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val Pro
87                      210                      215                      220
90 Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg Phe
91 225                      230                      235                      240
94 Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg His
95                      245                      250                      255
98 Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu Lys
99                      260                      265                      270
102 Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu Ser
103                      275                      280                      285
106 Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu Gly
107                      290                      295                      300
110 Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His Trp
111 305                      310                      315                      320
114 Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val Arg
115                      325                      330                      335
118 Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly Phe
119                      340                      345                      350
122 Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val Phe
123                      355                      360                      365
126 Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu Leu
127                      370                      375                      380
130 Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp Cys
131 385                      390                      395                      400
134 Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly Arg
135                      405                      410                      415
138 Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala Leu
139                      420                      425                      430
142 Trp Ala Val Leu Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr Leu
143                      435                      440                      445
146 Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg Pro
147                      450                      455                      460
150 Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro Ile
151 465                      470                      475                      480
154 Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg Arg
155                      485                      490                      495
158 Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val Val
159                      500                      505                      510
162 Met Cys Leu Val Ser Ile Ile Leu Tyr Arg Ala Ile Met Ala Ile Val
163                      515                      520                      525
166 Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg Ile
167                      530                      535                      540
170 Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile Leu

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171 545          550          555          560
174 Ser Lys Ile Tyr Val Ser Leu Ala His Val Leu Thr Arg Trp Glu Met
175          565          570          575
178 His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe Thr Leu Lys Val Phe
179          580          585          590
182 Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val Tyr Ile Ala Phe
183          595          600          605
186 Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr His Thr Leu Phe
187          610          615          620
190 Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly Cys Leu Ile Glu Leu
191 625          630          635          640
194 Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln Val Ile Asn Asn
195          645          650          655
198 Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp Trp Gln Lys Phe
199          660          665          670
202 Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser Ala Gly Ala Ser
203          675          680          685
206 Gln Gly Pro Trp Glu Asp Asp Tyr Glu Leu Val Pro Cys Glu Gly Leu
207          690          695          700
210 Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe Gly Phe Val Thr Ile
211 705          710          715          720
214 Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe Ala Leu Leu Asn Asn
215          725          730          735
218 Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe Val Cys Glu Tyr Arg
219          740          745          750
222 Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly Ile Trp Phe His Ile
223          755          760          765
226 Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn Ala Phe Leu Leu
227          770          775          780
230 Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr Tyr Arg Trp Thr Arg
231 785          790          795          800
234 Ala His Asp Leu Arg Gly Phe Leu Asn Phe Thr Leu Ala Arg Ala Pro
235          805          810          815
238 Ser Ser Phe Ala Ala His Asn Arg Thr Cys Arg Tyr Arg Ala Phe
239          820          825          830
242 Arg Asp Asp Asp Gly His Tyr Ser Gln Thr Tyr Trp Asn Leu Leu Ala
243          835          840          845
246 Ile Arg Leu Ala Phe Val Ile Val Phe Glu His Val Val Phe Ser Val
247          850          855          860
250 Gly Arg Leu Leu Asp Leu Leu Val Pro Asp Ile Pro Glu Ser Val Glu
251 865          870          875          880
254 Ile Lys Val Lys Arg Glu Tyr Tyr Leu Ala Lys Gln Ala Leu Ala Glu
255          885          890          895
258 Asn Glu Val Leu Phe Gly Thr Asn Gly Thr Lys Asp Glu Gln Pro Lys
259          900          905          910
262 Gly Ser Glu Leu Ser Ser His Trp Thr Pro Phe Thr Val Pro Lys Ala
263          915          920          925
266 Ser Gln Leu Gln Gln
267          930

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270 <210> SEQ ID NO: 2
271 <211> LENGTH: 3308
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
278 <400> SEQUENCE: 2
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281 ctcccctgcc tgcttcttgg ccacttgca ggcaagggtga gggcatgcga atggctgcca      120
283 ctgcctgggc ggggctccaa gggccacccc tccccaccct ctgtcccgca gtgaggacgg      180
285 gactctactg ccgagaccag gctcacgctg agagggtgggc catgacctcc gagacctctt      240
287 ccggaagcca ctgtgccagg agcaggatgc tgcggcgacg ggcccaggaa gaggacagca      300
289 ccgtcctgat cgatgtgagc ccccttgagg cagagaagag gggctcttac gggagcacag      360
291 cccacgcctc ggagccagggt ggacagcaag cggccgcctg cagagctggg agtcctgcca      420
293 agccccggat cgcagacttc gtctcgtttt gggaggagga cctgaagcta gacaggcagc      480
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299 cagtgcacta cgccctcctc agcgccctct gggctgtgct ctgctactac gccgaagacc      660
301 tgcgcctgaa gctgcccctg caggagttac ccaaccaggc ctccaactgg tcggccggcc      720
303 tgctggcatg gctgggcata cccaacgtcc tgctggagggt tgtgccagac gtaccccccg      780
305 agtactactc ctgcccgttc agagtgaaca agctgccacg ctctcctcggg agtgacaacc      840
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309 ccccgatatg ccacgagaag aaaaacctgc ttgggatcca ccagctgctg gcagagggtg      960
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319 tgggtgttct ggtgggctgc ttctgggtgt tctcagacat acccacgcag gaactgtgtg      1260
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341 ccttcacctt caagggtgtt atcttccagt tcgtcaactt ctactcctca cccgtctaca      1920
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349 agggctggtg gcagaagttc cggcttcgct ccaagaagag gaaggcgagg gcttctgcag      2160
351 gggctagcca ggggcccctg gaggacgact atgagcttgt gccctgtgag ggtctgtttg      2220
353 acgagtacct ggaaatggtg ctgcagttcg gcttcgtcac catcttcgtg gccgcctgtc      2280
355 cgctcgcgcc gctcttcgcc ctgctcaaca actgggtgga gatccgcttg gacgcgcgca      2340
357 agttcgtctg cgagtaccgg cgccctgtgg ccgagcgcgc ccaggacatc ggcacatcgt      2400
359 tccacatcct ggcgggcctc acgcacctgg cggtcacag caacgccttc ctcttgccct      2460
361 tctcgtccga cttcctgcgc cgcgcctact accggtggac ccgcgccac gacctgcgcg      2520

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363 gcttcctcaa cttcacgctg gcgcgagccc cgtcctcctt cgccgccgcg cacaaccgca 2580
365 cgtgcaggta tcgggctttc cgggatgacg atggacatta ttcccagacc tactggaatc 2640
367 ttcttgccat ccgcctggcc ttcgtcattg tgtttgagca tgggttttc tccgttgcc 2700
369 gcctcctgga cctcctggcg cctgacatcc cagagtctgt ggagatcaaa gtgaagcggg 2760
371 agtactacct ggctaagcag gcactggctg agaatgaggt tctttttgga acgaacggaa 2820
373 caaaggatga gcagcccaag ggctcagagc tcagctccca ctggacaccc ttcacggttc 2880
375 ccaaggccag ccagctgcag cagtgcagcc tggaaggaca tctggtggtc cttaggggag 2940
377 tggccctcc tgagccctgc gagcagcgtc cttttcctct tccctcaggc agcggctgtg 3000
379 tgaaccgctg gctgctgttg tgcctcatct ctgggcacat tgcctgcttc cccccagcgc 3060
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385 accctgtccc tcggtggcct ccccaggccc ctggacacga cagttctcct caggcagggtg 3240
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393 <211> LENGTH: 9
394 <212> TYPE: PRT
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398 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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402 Ser Leu Phe Met Ala Leu Trp Ala Val
403 1 5
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407 <211> LENGTH: 9
408 <212> TYPE: PRT
409 <213> ORGANISM: Artificial Sequence
411 <220> FEATURE:
412 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
414 <400> SEQUENCE: 4
416 Val Leu Leu Glu Val Val Pro Asp Val
417 1 5
420 <210> SEQ ID NO: 5
421 <211> LENGTH: 9
422 <212> TYPE: PRT
423 <213> ORGANISM: Artificial Sequence
425 <220> FEATURE:
426 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
428 <400> SEQUENCE: 5
430 Ala Leu Leu Ser Ala Ser Trp Ala Val
431 1 5
434 <210> SEQ ID NO: 6
435 <211> LENGTH: 9
436 <212> TYPE: PRT
437 <213> ORGANISM: Artificial Sequence
439 <220> FEATURE:
440 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
442 <400> SEQUENCE: 6
444 Leu Leu Ala Ile Arg Leu Ala Phe Val

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VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\10202005\J552515.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date